

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/073,064  
Source: 1FW/6  
Date Processed by STIC: 9/28/05

# ***ENTERED***

RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/073,064DATE: 09/28/2005  
TIME: 15:59:28

INPUT SET: S30741.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>
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1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4 (i) APPLICANT: Ciossek, Thomas  
5 Ullrich, Axel  
6 Millauer, Birgit  
7 (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS  
8 AND TREATMENT OF MDK1  
9 SIGNAL TRANSDUCTION  
10 DISORDERS  
11 (iii) NUMBER OF SEQUENCES: 12  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Lyon & Lyon  
14 (B) STREET: 633 West Fifth Street  
15 Suite 4700  
16 (C) CITY: Los Angeles  
17 (D) STATE: California  
18 (E) COUNTRY: U.S.A.  
19 (F) ZIP: 90071-2066  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
22 storage  
23 (B) COMPUTER: IBM Compatible  
24 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
25 (D) SOFTWARE: Word Perfect 5.1  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: US/10/073,064  
28 (B) FILING DATE: 12-Feb-2002  
29 (C) CLASSIFICATION: 435  
30 (vii) PRIOR APPLICATION DATA:  
31 (A) APPLICATION NUMBER: US/08/438,265  
32 (B) FILING DATE: MAY 9, 1995  
33 (A) APPLICATION NUMBER: US/08/368,776  
34 (B) FILING DATE: January 3, 1995  
35 (A) APPLICATION NUMBER: <Unknown>  
36 (B) FILING DATE: <Unknown>  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: Warburg, Richard J.  
39 (B) REGISTRATION NUMBER: 32,327  
40 (C) REFERENCE/DOCKET NUMBER: 208/007  
41 (ix) TELECOMMUNICATION INFORMATION:  
42 (A) TELEPHONE: (213) 489-1600  
43 (B) TELEFAX: (213) 955-0440  
44 (C) TELEX: 67-3510  
45 (2) INFORMATION FOR SEQ ID NO: 1:  
46 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/073,064DATE: 09/28/2005  
TIME: 15:59:28

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47 (A) LENGTH: 4304 base pairs  
48 (B) TYPE: nucleic acid  
49 (C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear  
51 (ii) MOLECULE TYPE: nucleic  
52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

53	AAGCGGCCGG	TCTGCAGTCG	GAGACTTGCA	GGCAGCAAAC	ACGGTGCGAA	50
54	CGAACCGGAG	GGGGGAGAGA	GAAATCAAAC	AGCTAAGCGT	GGAGCAGACG	100
55	GCCTGGGACC	CAGAAGGGGA	TCGATGCGAG	GAGCGCAATA	ATAACAACAA	150
56	TAATAACCCA	CTTCGGAGCA	AACAGCATCT	AAAGAGCTGC	GACCCAACTG	200
57	CAGCCTAAAA	AAATCAAACC	TGCTCATGCA	CCATGGTTGT	TCAAACCTCGG	250
58	TTCCCTTCGT	GGATTATTTT	GTGTTACATC	TGGCTGCTTG	GCTTTGCACA	300
59	CACGGGGGAG	GCGCAGGCTG	CGAAGGAAGT	ACTATTACTG	GACTCGAAAG	350
60	CACAACAAAC	AGAATTGGAA	TGGATTTTCT	CTCCACCCAG	TGGGTGGGAA	400
61	GAAATTAGTG	GTTTGGATGA	GAACACACT	CCGATAAGAA	CATACCAGGT	450
62	GTGCCAGGTC	ATGGAGCCCA	ACCAGAACAA	CTGGCTGCGG	ACTAACTGGA	500
63	TTTCTAAAGG	CAACGCACAA	AGGATTTTTG	TAGAATTGAA	ATTCACCTTG	550
64	AGGGATTGTA	ATAGTCTTCC	CGGAGTCCTG	GGAACCTGCA	AGGAAACGTT	600
65	TAATTTGTAC	TATTATGAAA	CAGACTACGA	CACCGGCAGG	AATATACGAG	650
66	AAAACCTTTA	TGTTAAAATA	GACACCATTG	CTGCAGATGA	AAGTTTCACA	700
67	CAAGGTGACC	TTGGTGAAAG	AAAGATGAAG	CTGAACACTG	AGGTGAGAGA	750
68	GATTGGACCT	TTGTCCAAAA	AGGGATTCTA	TCTTGCCTTT	CAGGATGTAG	800
69	GGGCTTGCAT	AGCATTGGTT	TCTGTCAAAG	TGTACTACAA	GAAGTGCTGG	850
70	ACCATTGTTG	AGAACTTAGC	TGTCTTTCCA	GATACAGTGA	CTGGTTCGGA	900
71	ATTTTCCTCC	TTAGTCGAGG	TCCGTGGGAC	ATGTGTCAGC	AGTGCCGAGG	950
72	AAGAGGCAGA	AAATTCCCCC	AGAATGCATT	GCAGTGCAGA	AGGAGAGTGG	1000
73	CTAGTACCCA	TTGGAAAATG	CATCTGCAAA	GCAGGCTATC	AGCAAAAAGG	1050
74	GGACACTTGC	GAACCCTGTG	GCCGCAGGTT	CTACAAATCT	TCCTCTCAGG	1100
75	ATCTCCAGTG	TTCTCGTTGT	CCAACCCACA	GCTTCTCTGA	CCGAGAAGGA	1150
76	TCATCCAGGT	GTGAATGTGA	AGATGGGTAC	TACAGAGCTC	CTTCTGATCC	1200
77	ACCATACGTT	ATCATGCACG	GGCCTCCCTC	TGCACCACAG	AACCTTATTT	1250
78	TCAATATCAA	TCAAACGACT	GTAAGTTTGG	AATGGAGTCC	TCCGGCTGAC	1300
79	AACGGGGGAA	GAAACGATGT	CACCTACAGA	ATACTGTGTA	AGCGGTGCAG	1350
80	TTGGGAACAG	GGAGAATGTG	TGCCATGCGG	AAGTAACATT	GGATACATGC	1400
81	CCCAGCAGAC	GGGATTAGAG	GATAACTATG	TCACTGTCAT	GGACCTACTT	1450
82	GCCCATGCAA	ATTACACTTT	CGAAGTTGAA	GCTGTAAATG	GAGTTTCGGA	1500
83	CTTAAGCAGA	TCCCAGAGGC	TCTTCGCTGC	TGTTAGCATC	ACCACCGGTC	1550
84	AAGCAGCTCC	CTCGCAAGTG	AGTGGAGTCA	TGAAGGAGCG	AGTACTGCAG	1600
85	CGGAGTGTGC	AGCTTTCCTG	GCAGGAGCCG	GAGCATCCCA	ATGGAGTCAT	1650
86	CACGGAATAT	GAAATCAAGT	ATTATGAGAA	AGATCAACGG	GAAAGGACGT	1700
87	ACTCAACACT	CAAAACCAAG	TCCACCTCCG	CCTCCATTAA	TAATCTGAAA	1750
88	CCGGGAACAG	TGTACGTCTT	TCAGATCCGG	GCGGTCACTG	CTGCCGGTTA	1800
89	TGGAAACTAC	AGCCCTAGGC	TTGATGTTGC	CACACTTGAG	GAAGCTTCAG	1850
90	GTAAATGTT	TGAAGCGACA	GCAGTCTCCA	GTGAACAGAA	TCCTGTCATC	1900
91	ATAATTGCTG	TAGTGGCTGT	AGCAGGGACC	ATCATCTTGG	TGTTTCATGGT	1950
92	GTTCCGGCTT	ATCATTGGAA	GAAGGCACTG	TGGTTATAGC	AAGGCTGACC	2000
93	AAGAAGGGGA	TGAAGAACTC	TACTTTTCATT	TTAAATTTCC	AGGCACCAAA	2050
94	ACCTACATTG	ACCCTGAAAC	CTATGAGGAC	CCAAATAGAG	CTGTCCATCA	2100
95	ATTCGCCAAG	GAGCTAGATG	CCTCCTGTAT	TAAAATTGAG	CGTGTGATTG	2150
96	GTGCAGGAGA	ATTTGGAGAA	GTTTGCACTG	GTGTTTGAA	ACTTCCGGGC	2200
97	CAGAGAGATG	TTGCAGTGCC	CATAAAAACC	CTGAAAGTTG	GTTACACAGA	2250
98	AAAGCAAAGG	AGGGACTTTT	TATGCGAAGC	AAGCATCATG	GGGCAATTTG	2300
99	ACCACCCAAA	TGTCGTCCAT	TTGGAAGGGG	TTGTTACAAG	AGGGAAGCCT	2350

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100	GTCATGATTG	TGATAGAGTT	CATGGAGAAT	GGAGCCCTGG	ATGCATTTCT	2400
101	CAGGAAACAC	GATGGGCAGT	TTACAGTCAT	TCAGTTGGTA	GGAATGTTGA	2450
102	GAGGTATTGC	CGCTGGGATG	CGATACTTGG	CTGATATGGG	ATACGTTTAC	2500
103	AGGGACCTTG	CAGCGCGCAA	CATCCTTGTC	AACAGCAATC	TTGTTTGTAA	2550
104	AGTGTGAGAT	TTTGGCCTTT	CCCGGGTTAT	AGAGGATGAT	CCCGAAGCTG	2600
105	TCTACACCAC	GACTGGTGGA	AAAATTCCAG	TAAGGTGGAC	TGCACCGGAA	2650
106	GCCATTCAAT	ACCGGAAGTT	CACCTCAGCC	AGCGATGTGT	GGAGCTATGG	2700
107	GATTGTCATG	TGGGAAGTGA	TGTCTTATGG	AGAAAGACCT	TACTGGGACA	2750
108	TGTCAAATCA	AGATGTCATT	AAAGCGATAG	AAGAAGGTTA	TCGTTTGCCG	2800
109	GCGCCCATGG	ATTGCCCAGC	TGGTCTTCAC	CAGCTAATGC	TGGATTGTTG	2850
110	GCAGAAAGAT	CGGGCGGAAA	GGCCAAAGTT	TGAGCAGATA	GTCGGAATTC	2900
111	TAGACAAAT	GATTCGAAAC	CAAGTAGTC	TGAAAACACC	CCTGGGAAC	2950
112	TGTAGTAGAC	CCTTAAGCCC	TCTTCTGGAC	CAGAGCACTC	CTGACTTCAC	3000
113	TGCCTTCTGT	TCAGTTGGAG	AATGGTTGCA	AGCTATTAAA	ATGGAAAGGT	3050
114	ATAAGGACAA	CTTCACAGCA	GCGGGTTACA	ACTCACTCGA	GTCAGTGGCC	3100
115	AGGATGACTA	TCGATGATGT	GATGAGTTTA	GGGATCACAC	TGGTTGGCCA	3150
116	TCAAAGAAG	ATCATGAGCA	GCATCCAGAC	TATGCGGGCA	CAAATGTTGC	3200
117	ATTTACACGG	AACAGGCATC	CAAGTGTGAC	ACATCGGCCT	CCCTCAGATG	3250
118	AGGCTTAAGA	CTGCAGGAGA	ACAGTTCTGG	CCTTCAGTAT	ACGCATAGAA	3300
119	TGCTGCTAGA	AGACAGTTGA	TATACTGGGT	CCTTCCTACA	AGAAAGAGAA	3350
120	GATTTTAGAA	GCACCTCCAG	ACTTGAAC	CTAAGTGCCA	CCAGAATATA	3400
121	CAAAAAGGGA	ATTTAGGATC	CACCACTGGT	GGCCAGGAAC	ACAGCAGAGA	3450
122	CAATAAACAA	AGTACTACCT	GAAAAACATC	CCAACACCTT	GAGCTCTCGA	3500
123	ACCTCCTTTT	TATCTTATAG	ACTTTTTTAA	AATGTACATA	AAGAATTTAA	3550
124	GAAAGAATAT	ATTTGTCAAA	TAAAAATCAT	GATCTTATTG	TTAAAATCAA	3600
125	TGAAATATTT	TCCTTAAAT	ATGTGATTTT	AGACTATTCT	TTTCCAGAAC	3650
126	CATCTGTGTT	TATTCTGCTT	AAGGACTTTG	TTTTAGAAAG	TTATTTGTAG	3700
127	CTTTGGACCT	TTTTAGTGTT	AAATTTATGA	CACGTTACTA	CACTGGGAAC	3750
128	CTTTGAAGAC	TCTCAAACTT	AAAGGAAAGC	AAAACACG	ACATAGTCGA	3800
129	GGATGGACTT	TGTCCTTCAT	GGCTTTGGTA	TCCTGGCTGT	GTCATTTTGT	3850
130	TAAACCAAGT	ATGTTTTCAT	ATTGTTTGCT	GATTGGCAGG	TAGTTCAAAA	3900
131	TTGCAAGTTG	CCAAGAGCTC	TGATATTTTT	TAACAGGATT	TTTTTTTCTT	3950
132	TGTAAAAATC	AGATAACATA	CTAACTTTTC	AATGAAAAAA	AAAAAAAAG	4000
133	AAGCAATAAT	GATCCATAAA	TACTATAAGG	CACTTTTAAC	AGATTGTTTA	4050
134	TAGAGTGATT	TACTAGGCAG	AATTTAATAA	AAAAAAAAGA	GAGATGTCAA	4100
135	ATTTTAGGTT	TATGTGTATA	TGATAAAAGG	CTGAGCTTCG	TCTGAAGATG	4150
136	CTGGTGAAAG	CAAGACTGGA	AGCGAAGCTC	TCCAGCTTTG	GCTAACCCAA	4200
137	TCCGAGCACA	TCAAGAGCTT	CAGTCTTG	ACAGTAAGAA	ATTTAGGAAC	4250
138	ATAGTTGACC	TATATTTTGT	ATTCTTTCTT	GTTGAATGCA	GTCCAAATAC	4300
139	AAAA					4304

140

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 998 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

149	Met	Val	Val	Gln	Thr	Arg	Phe	Pro	Ser	Trp	Ile	Ile	Leu	Cys	Tyr	Ile
150	1			5					10					15		
151	Trp	Leu	Leu	Gly	Phe	Ala	His	Thr	Gly	Glu	Ala	Gln	Ala	Ala	Lys	Glu
152				20					25						30	

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153	Val	Leu	Leu	Leu	Asp	Ser	Lys	Ala	Gln	Gln	Thr	Glu	Leu	Glu	Trp	Ile
154			35					40					45			
155	Ser	Ser	Pro	Pro	Ser	Gly	Trp	Glu	Glu	Ile	Ser	Gly	Leu	Asp	Glu	Asn
156		50					55					60				
157	Tyr	Thr	Pro	Ile	Arg	Thr	Tyr	Gln	Val	Cys	Gln	Val	Met	Glu	Pro	Asn
158	65					70					75					80
159	Gln	Asn	Asn	Trp	Leu	Arg	Thr	Asn	Trp	Ile	Ser	Lys	Gly	Asn	Ala	Gln
160				85					90					95		
161	Arg	Ile	Phe	Val	Glu	Leu	Lys	Phe	Thr	Leu	Arg	Asp	Cys	Asn	Ser	Leu
162			100					105						110		
163	Pro	Gly	Val	Leu	Gly	Thr	Cys	Lys	Glu	Thr	Phe	Asn	Leu	Tyr	Tyr	Tyr
164		115						120					125			
165	Glu	Thr	Asp	Tyr	Asp	Thr	Gly	Arg	Asn	Ile	Arg	Glu	Asn	Leu	Tyr	Val
166		130					135					140				
167	Lys	Ile	Asp	Thr	Ile	Ala	Ala	Asp	Glu	Ser	Phe	Thr	Gln	Gly	Asp	Leu
168	145					150					155					160
169	Gly	Glu	Arg	Lys	Met	Lys	Leu	Asn	Thr	Glu	Val	Arg	Glu	Ile	Gly	Pro
170				165						170					175	
171	Leu	Ser	Lys	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Val	Gly	Ala	Cys
172			180					185						190		
173	Ile	Ala	Leu	Val	Ser	Val	Lys	Val	Tyr	Tyr	Lys	Lys	Cys	Trp	Thr	Ile
174		195						200					205			
175	Val	Glu	Asn	Leu	Ala	Val	Phe	Pro	Asp	Thr	Val	Thr	Gly	Ser	Glu	Phe
176		210					215					220				
177	Ser	Ser	Leu	Val	Glu	Val	Arg	Gly	Thr	Cys	Val	Ser	Ser	Ala	Glu	Glu
178	225					230					235					240
179	Glu	Ala	Glu	Asn	Ser	Pro	Arg	Met	His	Cys	Ser	Ala	Glu	Gly	Glu	Trp
180				245						250					255	
181	Leu	Val	Pro	Ile	Gly	Lys	Cys	Ile	Cys	Lys	Ala	Gly	Tyr	Gln	Gln	Lys
182			260					265						270		
183	Gly	Asp	Thr	Cys	Glu	Pro	Cys	Gly	Arg	Arg	Phe	Tyr	Lys	Ser	Ser	Ser
184		275						280					285			
185	Gln	Asp	Leu	Gln	Cys	Ser	Arg	Cys	Pro	Thr	His	Ser	Phe	Ser	Asp	Arg
186		290					295					300				
187	Glu	Gly	Ser	Ser	Arg	Cys	Glu	Cys	Glu	Asp	Gly	Tyr	Tyr	Arg	Ala	Pro
188	305					310					315					320
189	Ser	Asp	Pro	Pro	Tyr	Val	Ala	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	Gln
190				325						330					335	
191	Asn	Leu	Ile	Phe	Asn	Ile	Asn	Gln	Thr	Thr	Val	Ser	Leu	Glu	Trp	Ser
192			340					345						350		
193	Pro	Pro	Ala	Asp	Asn	Gly	Gly	Arg	Asn	Asp	Val	Thr	Tyr	Arg	Ile	Leu
194		355						360					365			
195	Cys	Lys	Arg	Cys	Ser	Trp	Glu	Gln	Gly	Glu	Cys	Val	Pro	Cys	Gly	Ser
196		370					375					380				
197	Asn	Ile	Gly	Tyr	Met	Pro	Gln	Gln	Thr	Gly	Leu	Glu	Asp	Asn	Tyr	Val
198	385					390					395					400
199	Thr	Val	Met	Asp	Leu	Leu	Ala	His	Ala	Asn	Tyr	Thr	Phe	Glu	Val	Glu
200				405						410					415	
201	Ala	Val	Asn	Gly	Val	Ser	Asp	Leu	Ser	Arg	Ser	Gln	Arg	Leu	Phe	Ala
202			420					425						430		
203	Ala	Val	Ser	Ile	Thr	Thr	Gly	Gln	Ala	Ala	Pro	Ser	Gln	Val	Ser	Gly
204		435						440					445			
205	Val	Met	Lys	Glu	Arg	Val	Leu	Gln	Arg	Ser	Val	Gln	Leu	Ser	Trp	Gln

**INPUT SET: S30741.raw**

206	450					455					460									
207	Glu	Pro	Glu	His	Pro	Asn	Gly	Val	Ile	Thr	Glu	Tyr	Glu	Ile	Lys	Tyr				
208	465					470					475					480				
209	Tyr	Glu	Lys	Asp	Gln	Arg	Glu	Arg	Thr	Tyr	Ser	Thr	Leu	Lys	Thr	Lys				
210	485					490					495									
211	Ser	Thr	Ser	Ala	Ser	Ile	Asn	Asn	Leu	Lys	Pro	Gly	Thr	Val	Tyr	Val				
212	500					505					510									
213	Phe	Gln	Ile	Arg	Ala	Val	Thr	Ala	Ala	Gly	Tyr	Gly	Asn	Tyr	Ser	Pro				
214	515					520					525									
215	Arg	Leu	Asp	Val	Ala	Thr	Leu	Glu	Glu	Ala	Ser	Gly	Lys	Met	Phe	Glu				
216	530					535					540									
217	Ala	Thr	Ala	Val	Ser	Ser	Glu	Gln	Asn	Pro	Val	Ile	Ile	Ile	Ala	Val				
218	545					550					555					560				
219	Val	Ala	Val	Ala	Gly	Thr	Ile	Ile	Leu	Val	Phe	Met	Val	Phe	Gly	Phe				
220	565					570					575									
221	Ile	Ile	Gly	Arg	Arg	His	Cys	Gly	Tyr	Ser	Lys	Ala	Asp	Gln	Glu	Gly				
222	580					585					590									
223	Asp	Glu	Glu	Leu	Tyr	Phe	His	Phe	Lys	Phe	Pro	Gly	Thr	Lys	Thr	Tyr				
224	595					600					605									
225	Ile	Asp	Pro	Glu	Thr	Tyr	Glu	Asp	Pro	Asn	Arg	Ala	Val	His	Gln	Phe				
226	610					615					620									
227	Ala	Lys	Glu	Leu	Asp	Ala	Ser	Cys	Ile	Lys	Ile	Glu	Arg	Val	Ile	Gly				
228	625					630					635					640				
229	Ala	Gly	Glu	Phe	Gly	Glu	Val	Cys	Ser	Gly	Arg	Leu	Lys	Leu	Pro	Gly				
230	645					650					655									
231	Gln	Arg	Asp	Val	Ala	Val	Ala	Ile	Lys	Thr	Leu	Lys	Val	Gly	Tyr	Thr				
232	660					665					670									
233	Glu	Lys	Gln	Arg	Arg	Asp	Phe	Leu	Cys	Glu	Ala	Ser	Ile	Met	Gly	Gln				
234	675					680					685									
235	Phe	Asp	His	Pro	Asn	Val	Val	His	Leu	Glu	Gly	Val	Val	Thr	Arg	Gly				
236	690					695					700									
237	Lys	Pro	Val	Met	Ile	Val	Ile	Glu	Phe	Met	Glu	Asn	Gly	Ala	Leu	Asp				
238	705					710					715					720				
239	Ala	Phe	Leu	Arg	Lys	His	Asp	Gly	Gln	Phe	Thr	Val	Ile	Gln	Leu	Val				
240	725					730					735									
241	Gly	Met	Leu	Arg	Gly	Ile	Ala	Ala	Gly	Met	Arg	Tyr	Leu	Ala	Asp	Met				
242	740					745					750									
243	Gly	Tyr	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser				
244	755					760					765									
245	Asn	Leu	Val	Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Ile	Glu				
246	770					775					780									
247	Asp	Asp	Pro	Glu	Ala	Val	Tyr	Thr	Thr	Thr	Gly	Lys	Ile	Pro	Val					
248	785					790					795					800				
249	Arg	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Gln	Tyr	Arg	Lys	Phe	Thr	Ser	Ala				
250	805					810					815									
251	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Val	Met	Trp	Glu	Val	Met	Ser	Tyr				
252	820					825					830									
253	Gly	Glu	Arg	Pro	Tyr	Trp	Asp	Met	Ser	Asn	Gln	Asp	Val	Ile	Lys	Ala				
254	835					840					845									